

RNA target sequence present in each member of said set. The approach is based on oligonucleotide hybridization probes complementary to RNA sequences that are diagnostic for selected phylogenetic groups which correspond, to varying degrees, to a target region typical of a type of a microorganism or a whole group of microorganisms. Any probes enabling said contacting step is appropriate for the implementation of the method according to the invention. The choice of the specific probe(s) is directly related to the analysis desired for said sample. Probes can *e.g.* be composed of oligonucleotide sequences that can distinguish between the primary kingdoms (eukaryotes, eubacteria, archaebacteria) and between closely related organisms (the group of Ammonia-oxidizing β -Proteobacteria, the genus *Nitrobacter* or *Acinetobacter* or the species *Fibrobacter intestinalis*, the species *Escherichia Coli*). Probes with finer phylogenetic resolution can be derived by using the existing collections of RNA sequences. Many examples of such RNA-targeted probes are described in the prior art such as patents or patent applications, scientific publications *e.g.* Los Reyes *et al.* 1997, *Appli. Environ. Microbiol.* Vol. 63 No. 3 p.1107-1117 ; Mobarry *et al.* 1996, *Appli. Environ. Microbiol.* Vol. 62 No. 6 p.2156-2162 ; Wagner *et al.* 1994, *Appli. Environ. Microbiol.* Vol. 60 No. 3 p.792-800 ; Kane *et al.* *Appli. Environ. Microbiol.* Vol. 59 No. 3 p.682-686. Other examples of such probes can also be designed by the person skilled in the art. Advantageously probes are those which target ribosomal RNA (rRNA). Examples of such advantageous probes include Nb1000 (SEQ ID No. 1) and Nso 1225 (SEQ ID No. 2).

Page 11, second paragraph should read as follows:

c) Hybridization step

A water bath is prepared at the hybridization temperature required by the probe being used (the temperature depends on the length and sequence of the probe). In the example reported here, the following probes were used:

Probe Nb 1000 specific to the *Nitrobacter* genus, with sequence SEQ ID No. 1:
5' TGCGACCGGTCATGG 3'

Probe Nso 1225, specific to Ammonia-oxidizing β proteobacteria, with sequence
SEQ ID No. 2: 5' CGCCATTGTATTACGTGTGA 3'

Probe S Univ-1390, a universal probe for any microorganism, with sequence SEQ ID No. 3: 5' GACGGGCGGTGTGTACAA 3', and

Probe S Bac338, specific for bacteria, with sequence SEQ ID No. 4:
5' GCTGCCTCCCGTAGGAGT 3'.

Pages 18 and 19, titled LIST OF SEQUENCES should read as follows:

LIST OF SEQUENCES

(1) General information:

- (i) Applicant:
 - (a) Name: Suez Lyonnaise des Eaux
 - (b) Address: 72 avenue de la Liberté
 - (c) City: Nanterre Cedex
 - (e) Country: France
 - (f) Postal code: 92753
- (ii) Title of the invention: Means for qualitative and quantitative analysis of the microbial populations potentially present in a sample
- (iii) Number of sequences: 4
- (iv) Form readable by computer:
 - (a) type of storage medium: floppy disk
 - (b) computer: IBM PC compatible
 - (c) operating system: PC-DOS/MS-DOS
 - (d) software: PatentIn Release #1.0, Version #1.30 (OEB)

(2) Information for SEQ ID No. 1:

- (i) Characteristics of the sequence:
 - (a) Length: 15 base pairs
 - (b) Type: nucleotide
 - (c) Number of strands: single
 - (d) Configuration: linear
- (ii) Type of molecule: other nucleic acid
- (iii) Hypothetical: yes
- (iv) Antisense: no
- (vii) Immediate source:
 - (B) Clone: Nb1000
- (xi) Description of the sequence: SEQ ID No. 1:
TGCGACCGGT CATGG

(3) Information for SEQ ID No. 2:

- (i) Characteristics of the sequence:
 - (a) Length: 20 base pairs
 - (b) Type: nucleotide
 - (c) Number of strands: single

- (d) Configuration: linear
 - (ii) Type of molecule: other nucleic acid
 - (iii) Hypothetical: yes
 - (iv) Antisense: no
 - (vii) Immediate source:
(B) Clone: Nb1225
 - (xi) Description of the sequence: SEQ ID No. 2:
5' CGCCATTGTA TTACGTGTGA 3'
- (4) Information for SEQ ID No. 3:
- (i) Characteristics of the sequence:
 - (a) Length: 18 base pairs
 - (b) Type: nucleotide
 - (c) Number of strands: single
 - (d) Configuration: linear
 - (ii) Type of molecule: other nucleic acid
 - (iii) Hypothetical: yes
 - (iv) Antisense: no
 - (vii) Immediate source:
(B) Clone: S Univ-1390
 - (xi) Description of the sequence: SEQ ID No. 3:
5' GACGGGCGGTGTGTACAA 3'
- (5) Information for SEQ ID No. 4:
- (i) Characteristics of the sequence:
 - (a) Length: 18 base pairs
 - (b) Type: nucleotide
 - (c) Number of strands: single
 - (d) Configuration: linear
 - (ii) Type of molecule: other nucleic acid
 - (iii) Hypothetical: yes
 - (iv) Antisense: no
 - (vii) Immediate source:
(B) Clone: S Bac338
 - (xi) Description of the sequence: SEQ ID No. 4:
5' GCTGCCTCCCGTAGGAGT 3'